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cgactggagcacgaggacactgacatggactgaaggagtagaaaggtttaaaaaacccagtttgagaa ATG TCT AAG TCT GGG CTT CAT CTT M S KSGLHL GTA GCC TAC ATA TTA TTG ATA TTT TTA ATT TCA ACT AAT ATA GCA TCT AAA ATT TCT GGT GTT CCA TTA TGC AAC V A Y I L L I F L I S T N I A S K I S G V P L C N 168 AAA GAT ACT TCA CCA GTA TTT ACA CTT CAA CAT AAT TCT ACT AAT GGT ATT TTA GCT AGA TCT CTT CCA CAA CCA V F T L Q H N S T N G I L A R S L P S P 243 GGA TTA ATT GAT TGT TCA GAA CAT TGT TCC TCT TCG TCA GAT TGT ATT GGC GTT GAA TAT TGG CAG GGA ATT TGT D C S E H C S S S S D C I G V E 318 AGA GTT ATT TCT CAA GAT AAA ACT TCT ATT TAT ACA CCA ACA GAT GAA ACT TCA ATA CTT TTA ACA AAA TCA TGT PTDETS RVISQDKTS I Y T ILLTKSC GTT AAA AGT GAT CGT ATA TGT TCA TCA CCA TTC CAT TTT GAT GTT TAT GAA CAA AAA ATA TTA GTT GGA TTT GCT D R I C S S P F H F D V Y E Q K I L V G v K 468 AGA GAA GTT GTA CCA GCT GAG TCT ATT GAA ATT TGT ATG GCT GCT TGT TTG AAT GCT TTT GAT ACA TAT GGT TTT PAESIEICMAA СЬ N Α 543 GAA TGT GAA TCA GCT ATG TAT TAT CCA GTT GAT AGT GAA TGT ATT CTT AAT ACT GAA GAT AGA CTT GAT CGA CCA ECESAMYYPVDSECILNTEDRLDRP 618 V V E K E D V V Y Y L D S N C A G S Q C D L 693 CCA TAC ATT ACA CAA TAT ATT GCT GTT GAA AAT AAA CAA ATA GAA AAT GAA TTA GAT AGA AAA TTT GAA AAT ATT PYITQYIAVENKQIEN E L D GAT TTC CAA ACA TGT GAA GAA TTA TGT ACT GGT AGA ATT ACT GTT ACA CAA AAT GAT TTT ACT TGT AAA TCA TTT D F Q T C E E L C T G R I T V T Q N D F T C K S F 843 ATG TAT AAT CCT GAA ACA AAA GTT TGT TAT CTT TCT GAT GAA CGT TCA AAG CCT CTT GGA CGG GCT AAA TTA AGT PET K V C Y L S D E R S K P L G R A K L S 918 GAT GCT AAT GGA TTT ACT TAT TAT GAA AAA AGA TGT TTT GCA TCT CCA AGA ACA TGC CGT CAA ACA CCA TCA TTT YYEKKCFASP R T C R DANGFT 993 AAT AGA GTA CCA CAA ATG ATT CTT GGT GGT TTT GCT GCA TTT GTT ATG GAA AAT GTA CCA TCT GTT ACT ATG TGC N R V P Q M I L V G F A A F V M E N V P S V T CTT GAT CAA TGT ACA AAT CCA CCA GAG ACA GGT GAA AAA TTT GTC TGT AAA TCT GTT ATG TAC TAT TAT AAT Q C T N P P P E T G E K F V C K S V M Y Y 1143 GAA CAA GAA TGT ATT CTT AAT GCT GAA ACA AGA CAT ACA AAG CCA GAT CTT TTT ATT ACA GAA GGA GAT GAA TTT EQECILNAETRHTKP D L F I 1218 CTT GTT GAT TAT TTT GAT ATT TCA TGT CAT CTT GAA CCA GAA ACA TGT CCT AAA GGA ACA TAT TTA AAA GGA ATT LVDYFD I S C H L E P E T C P K G T Y L K G I 1293 AAA TCT ATC AAT TCT GCA CTT CCT GAG GGT GAA GGC TCA CTT CAT GTT ATT GAG TCT GCT GGA AAA TCA TTA GAA N S A L P E G E G S L H V I E S A G K S 1368 GAA TGT ATG GAA AAA TGT AAC CAA CTT CAT CCA GAA AAA TGT AGA TCA TTT AAT TTT GAA AAA TCA TCT GGA TTA ECMEKCNQLHPEKCR S F N E S 1443 TGT AAT CTT TTA TAT CTT GAT GGA AAA AAT ACT TTA AAA CCA TTT ATT AAA AAT GGA TTT GAT CTT GAT TTA C N L L Y L D G K N T L K P F I K N G F D L V D L

FIG. 1A

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CAA TGT TTA TCA ACT AAA AAA GAT TGC TCT ACA AAA AAG AAT GAT ATT AAT TTT GTT AAA TAT CTT TAC TCT CAT O C L S T K K D C S T K K N D I N F V K Y L Y S H 1593 TTT GTT AAA TAT CTT TAC TCT CAA CAA CCT GGA ATT CCA ACA AAA ACA GAA AAA GTT ATT GGT ATT TCT AAA TGT Y L Y S Q Q P G I P T K T E K V I G 1668 CTT GAT TTA TGT ACT GAT AGT GAA CGT TGT GAA GGA CTT AAT TAT AAT AGA AGA ACT GGA GAA TGT CAA TTA TTT L D L C T D S E R C E G L N Y N R R T G E C Q L 1743 GAA ATT ATT GAT GGA CCT TCT AAT CTT AAA AAA TCT GAG CAT ATA GAT TTT TAT CAA AAT CTT TGT TCT ACT AAA EIIDGPSNLKKSEHIDFYQNLCSTK 1818 GAA AAT GAA GCT GGT GTT TCA TCT GCA TTA AAT GTA CCA CAA TCA TCT GTT ATT CCT ATT TCA TCA TCA CAA AAT ENEAGVSSALNV PQSSVIPISSSQN 1893 ATT AGT AAA AGT GAT GTT TTT GCC AAA AAA AAT CTT AAT AAA GAT GGT AAT AAT CAA GTA AAC ATT TAT GAA CCA I S K S D V F A K K N L N K D G N N Q V N GAA AAA AAA TAC CAT CCA AAA GGA TCA AAA AAT GAA ACA TCA TAT GAA ACA GGA ACT GTA AAT AAA TCA AAT GTT E K K Y H P K G S K N E T S Y E T G T V N K S N V 2043 GAA GAG GTT TCT GAA ACT TTA ACT AAT AGT GGA GTT GAA AGT GGA AGT CTT GAA AAA AAT ATT ACA GCA CCA ETLTNSGVESGSLE S KNIITA 2118 CCA TCT ATA CCA AAA ATT CCT GAA GGT CCA CTA CCA GTG CCA ATT TTA ATT CCA GCT GAT CAA GTA CAA ACT ATT P S I P K I P E G P L P V P I L I P A D Q V Q 2193 TGT GAT TAT GAA GGT ATT AAA GTA CAA ATT AAA TCA CCA CAA TCA TTT ACT GGT GTT ATC TTT GTT AAA AAT CAC C D Y E G I K V Q I K S P Q S F T G V I F V K N H 2268 TAT GAA ACA TGT CGT GTT GAA GTT TCC AAC TCT GAT GCA GCT ACT CTT GAG CTT GGT CTT CCA GCT TCA TTT GGA Y E T C R V E V S N S D A A T L E L G L P 2343 ATG AAA CCA GTT ACA CTG TCT GCT ACA TCT TCA GAT TCT ACC TCT TCA CAG AAT ATT ACT TCT AAT AGT GGA CAT M K P V T L S A T S S D S T S S Q N I T S N S AAA GTT GTT GGA AGA GCA CGC CGT GAT ACA CAA GAA AAA TCT TGT GGT CTT ACA GAA ATT GAA AAT GGA AAA TAT RARRD TQEKSCGLTEIENG 2493 AAA AGT ACT GTT GTT ATA CAA ACA AAT AAC CTT GGA ATT CCT GGA CTT GTA ACA TCA ACA GAT CAA ATT TAT GAA I P G L V T S T D Q I K S T V V I Q T N N L G 2568 I G C D Y S S M L G G K I T T A A N M T CCA ACT GAT ATT AAA CCT AGA GGT AAA ATT GAA CTT GGA AAT CCT GTT CTT ATG CAA ATG AAT GCT GGT ACA GGT P T D I K P R G K I E L G N P V L M Q M N A G 2718 GAT CAT CAG CCA ATT TTA CAA GCT AAA CTT GGA GAT ATT CTT GAA TTA AGA TGG GAA ATT ATG GCT ATG GAT GAA ILELRW EIMAM ILQAKLGD 2793 GAA CTT GAT TTC TTT GTT AAA GAT TGT CAT GCA GAA CCT GGT ACT GGT GCT GGA GGA GAA GAA CTT CAG CTT ELDFFVKDCHAEPGTGAGGDEKL IKLOS GGCPT PAVAQKLI P Q P I E 2943 GTC AAA ATT GCC CAT CTT CAA GCT TTC CGT TTT GAT TCA TCC TCT TCA GTT AGA ATA ACA TGT AAT ATT GAA ATT SSSSVRITCNI HLQAFRFD 3018 TGT AAG GGA GAT TGT AAA CCA GCA ACA TGT GAT ATG CAC GGA GAA TCA AAA CAA TCA TGG GGA AGA AAA AAG AGA C K G D C K P A T C D M H G E S K Q S W G R K K R CAT ATT GAA GAT GAT ACA ATT ACA GAA TTT GAG ACA AAT CGT TAT AAA GTT CCA AGA TTT TCA CAA GCA ACA ACA N R Y K V P R F S Q A F E T T E

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31168
TCT CTT TTA ATT CTT GAT CCA GAT CCA CTT CAA AAT AAC ATT GAA CCA GCA TCA TTA ATG TCA AAA GTA CTT CTT GAT S L L I L D P L Q N N N I E P A S L M S K V S S L D ATG TTA GCT TTA GCT TTA GCT TTA GCT GAA CCA TTA ATG TCA TCT TCT TCA ATG TCA ATG TCA TCT TCT TCA ATG TCA ATG

FIG. 1C

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ggcacgagaa ATG AAC TGG CTA TCT ATA GCT TCA ATT TGT ACA TTC TTA ATT ATA CCA ATA TCT GCT GTC TTT GAA
        M N W L S I A S I C T F L I I P I S A V F E
TGT TCA GGA TCA GAA ACT ACA GCA TTT ATT AGA ATA TCC AGA GCA CGC CTT GAT GGG ACA CCA GTA GTT ATT TCT
     G S E T T A F I R I S R A R L D G T P
152
ACA GCA GGA CAT GAC TTG ACT TGT GCA CAA TAT TGT AGA AAT AAT ATT GAA CCA ACA ACT GGT GCT CAA CGT GTC
              L T C A Q Y C R N N I E P T T G A Q
TAGHD
TGT GCA TCA TTT AAT TTT GAT GGT CGT GAA ACA TGC TAC TTT TTT GAT GGT GCC TCA CCT GCT GGG ACT GGG
              F D G R E T C Y F F D D A A S P A G T G
CASFN
GAG TTG AAT GAA GCA CCA TCA GCT AAT AAT TTT TAT TAT GAA AAA GTT TGC CTT CCA GCT ATC TCT GCT CAT GAA
ELNEAPSANNFYYEKVCLPAISAHE
377
GCA TGT ACT TAT AGA TCA TTT TCA TTT GAA AGA ACT AGA AAT ACT CAA TTA GAA GGT TTT GTT AAA AAA TCA CTA
       Y R S F S F E R T R N T Q L E G F V K K S
ACT
452
CAA GTT ACA TCA CGT GAA GAA TGC CTT TCT ACA TGT TTA AAA GAA AGT GAA TTT GTA TGT AGA TCA GTT AAC TAT
                                C L K E S E F V C R S V N Y
        s
           R
              EECL
                          s
                             T
527
AAT TAT GAA AAC TTT ATG TGT GAA CTT TCA ACA GAA AGA TCG CGT TCT AAA CCA CAA AAT ATG AGA ATG TCA GCA
NYENFMCELSTERSRSKPQNMRMSA
602
GCT CCA GTT GAT TAT TAT GAT AAT AAT TGT TTA AAT AGA CAA AAT AGA TGT GGT GAA TCT GGT GGA AAT TTG ATT
     V D Y Y D N N C L N R Q N R C G E S
                                                          G G N
A P
TTT ATT AAA ACA ACA CAA TTT GAA ATT CAT TAT TAT GAT CAT ACT CAA TCA ATG GAA GCA CAA GAA TCA TTC TGT
              Q F E I H Y Y D H T Q S M
                                                    EAQES
FIKTT
752
TTA CAA AAA TGT TTA GAT TCA TTA AAC ACC TTC TGT AGA TCT GTT GAA TAT TCT CCA TCT GAA AAA AAT TGT ATT
L Q K C L D S L N T F C R S V E Y S P S E K N C I
827
GTT TCT GAT GAA GAT ACA TAT TCA AGA GCT GAT CAA CAA GGT GAA GTT AAT AAA GAT TAT TAT GAA CCT GTT
V S D E D T Y S R A D Q Q G E V N N K D Y Y E
902
TGT GTT GCT GCT GAT CTT AGT TCA TCT ACA TGT CGT CAA CAA GCT GCT TTT GAA AGA TTT ATT GGT TCT GCT ATT
C V A A D L S S S T C R Q Q A A F E R F I G S A I
GAA GGT ACC CCA GTT GCT ACA GCA CAA CAA GTA ACC ATT TCT GAT TGT ATT TCA CTT TGT TTC CAA AAT TTG AAT
EGTPVATAQQVTISDCISLC
1052
TGT AAA TCA ATT AAT TAT GAT CGT ACA CAA TCT ACA TGT TAT ATT TAT GCT GTT GGA AGA CAA GAA TCT AAT GTT
C K S I N Y D R T Q S T C Y I Y A V G R Q E S N V
AAA AAT GAT GCA AGT TTC GAT TAT TAT GAA TTT ACA ATT ATT GAT AAT GGA TGC CCA AGA TAT CCT GCT CTT GTA
                            F
                                     I D N G C P R Y P A
                    Y Y E
                               T
                                  I
KNDASF
                 D
1202
GGG CCA GTT TTA CAA GAT TTC GAC AAA AAT CGT CTT AAA TCT GAA ATG AAA GCA TTC CGT TTA GAT GGA TCA TAT
G P V L Q D F D K N R L K S E M K A F R L D G
1277
GAT ATT CAA ATT GAA TGT TCT GTT ATG TTT TGT GCT GGT CCA ATG GGT TGT CCA CCA TCT AAT TGC CTT GAT TCA
       I E C S V M F C A G P M G C P P S
DIQ
1352
GGA ACA AAT GAA TTA TTT GCT TCA CAT GGA AGA AAG AAA AGA AGT ATT GTT GAT TTC AAA AAT ACA ACA ACA TCT
G T N E L F A S H G R K K R
                                         S
                                           I
                                              v
                                                 D
                                                    F K N
                                                              т т
GCA GAA ACA TTA TCT GCT ATA ATT AGA GTA CTT GCT GCT GGA GAA GAA GAA GTA GAA GTT GAA GAA TTT TAT AGA
A E T L S A I I R V L A A G E E L E V E E F Y R
1502
AAT GAT ACT AAT TTT AAA TAT GAT TCT GAA GAA AAT ATC TCA GCT CAT AAC TTA TAC TGT ATG TCT GAA ATG TGG
       N F K Y D S E E N I S A H N L Y C M S E M W
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1577
TTT GTA GGA ATT GTA GGA ATT GTA GGA ATT GTA ATG GCA ATG G

FIG. 2B

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101 MVTKI CCA ACT TTT CCC CTC CTT TTT ATT TTC CCA TTT TTA TTT ACA TTT TTA ACG ACA AAA TGT CAG GCT TAT TCT ATA PTFPLLFIFPFLFTT K C Q A Y S 271 CCA TTA ATA TCA GAA TGT AAT TCG GAA GAA GCC CCA GTT TTT CTT TTG CAA CGG AAT GTT TCT TCT ATC GCC GGA P L I S E C N S E E A P V F L L Q R N V S S I A G ACT GAG CCT TTA AGA ACT GTT CCT GTT ACA GGG GGA TTT TTG GAA TGT GCG GAA CTT TGT TCA GCA GCA AAT AAT L R T V P V T G G F L E C A E L C S A A N N 421 TGT GTT GCT GTT AAA TTT TCT ATT GAA AAA CAA TGC CAA TTG TTG GGG AAA ACA ACT ATG ACA GCA ACA ACT TTA CVAVKFSIEKQCQLLGKTTMTAT 496 TCT TTA CAA GAC ATT AAT TTG ACA CTA GCT AGA TTA GCT ACT AAA AGT TGT GTT AAG AGC AAA AAA ATC TGT TCT S L Q D I N L T L A R L A T K S C V K S K K I TCC CCC TTC CAT TTT GAT GTT CAC GAA CAA AAA ATA CTT GTT GGT TTT GCT AGA GAA GTT GTA TCA GCA GAA TCT S P F H F D V H E Q K I L V G F A R E V V S A E S 646 ATA CAT CAA TGT TTA ACT GCT TGT TTA GAT GCT GTT GAT ACT TTT GGC TTT GAA TGC GAG TCA GTA ATG TAT TAT I H Q C L T A C L D A V D T F G F E C E S V M CCA TTG GAT GCC GAA TGT ATT TTA AAT ACA GAA GAC AGA CTT GAC CGT CCA GAT TTG TTT GTT GAT GAG AAG GAA PLDAECILNTEDRLDRPDLF 796 GAT ACT GTT GTT TAT TTG GAT AAT AAT TGT GCT GGA TCC CAA TGT CAT GCC CCT TAT GTA ACC CAA TAT GTA GCT D T V V Y L D N N C A G S Q C H A P Y V T Q Y V A 871 GTT GAA GGA AAA CAA TTA GCT GAG GAA TTG GAT CAT AAT TTT GAG GGA ATG GAG TTG ACA GAA TGT GAA CAG CTT V E G K Q L A E E L D H N F E G M E L T E C E Q L 946 TGT AAT CAA AGA TTG AGT GTT TCT GCA AAT GAC TTT AAT TGC AAA GCA TTT ATG TAC AAT AAC CAA ACA AGA TCT C N Q R L S V S A N D F N C K A F M Y N N Q T 1021 TGT ATT CTT TCT GAT GAA CGT TCA AGA CCT TTG GGT AGA GCT AAT TTG ACA GAT GCT AAA GGA TGG ACT TAT CAC CILSDERSRPLGRANLTDAKGWTYH 1096 GAG AAA AAA TGT TTT GCC TCC CCA CGT ACA TGC CGA AAT GTT CCT TCT TTT ACC CGC GTC CCT CAA ATG TTA TTA E K K C F A S P R T C R N V P S F TRVPQMLL GTT GGA TTT GCC TCT TTT GTA ATG GAA AAT GTC CCT TCA GTA ACT ATG TGT TTG GAT CAA TGT ACA AAT CCT CCC V G F A S F V M E N V P S V T MCLDQCTN 1246 CCA GAA ACT GGA CAA AGT TTT GTT TGT AAA TCT GTC ATG TAT TAT TAT AAT GAG CAA GAA TGT ATT TTA AAT GCT G Q S F V C K S V M Y Y Y N E Q E C I L N 1321 GAA TCA CGT CAT TCC AAG CCA GAT TTA TTT ATT CCC GAA GAA GAC GAT TTT GTT GTA GAT TAT TTT GAT ATA AAT E S R H S K P D L F I P E E D D F V V D TGC CGT CTA GAA CAA GAA CAA TGT ATC GAT GGA AGA ACG CCC CAA TTA GTT AGA ACA ATT AAT TCT GCA CTT CCA CRLEQEQCIDGRTPQLV RTINSA 1471 GAA GGG GAG GGG TCT ATA CAT GTT TTG GAA ACA ATT AAG GGA GGA GTT CAG CAA TGT GCT AAA AAA TGT TCT GAA G S I H V L E T I K G G V Q Q C A K K C S E E G E 1546

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CGC GCC CCA GAC AAA TGT CGC TCT TTC AAT TTT GAT AAA CAA GCT GGT AAT TGT AAT TTA CTT TAT TTG GAT GGA A P D K C R S F N F D K Q A G N C N L L Y L D R 1621 CAA GGG TCT TTA CGA CCA GAG CAA AAG ACA CAA TTC GAT TTA TAC GAT GTT CAT TGT TTG AGT GGA ACA TCT CAA LRPEQKTQFDLYDVHCL 1696 CTT TTA GGA GAA AAT TCT AAA CAT TCT CCC TCT GCT TGT GTC GAC CCA GAA GGG GCT ATT TTT AGT CGT TTC CTC G E N S K H S P S A C V D EGAIFSRFL L L 1771 TAC ACT CGT TGG GTA GCA AAT TCT CCC AAT CGT GAA ATT TCA AGT TTA CCA CTT TCC AAA TGT TTA AAT CTT TGT R W V A N S P N R E I S S L P L S K C L N L C т 1846 TCG GTT GGA GGA GAA CAA TGT GAG GGT GTT AAT TAC AAT CGC CGA AAT GGT TCT TGT CAA TTA TTT ACT TCC CTT G E Q C E G V N Y N R R N G S C Q L F T S L 1921 N S S P N S Q Q D K D E H V D F Y R N I C R AAG GAA TCG AAA AGT GAT AGT GGG GCT GCT AAT GTA CCC AAA ACA CAA CAA GCA ACG GCT GCA CCT CCC CCT TCT S K S D S G A A N V P K T Q Q A T A A P 2071 GTT CAA TTA ACT ACT AAA CCT CCA CAA ATT CGT GAT TTA AAC AAC AAC AAA ACA ACA CAC AAA GAA CCA AAT Q L T T K P P Q I R D L N N N N K T T H K E P 2146 ATT AAA CTT CCA CCA CAA TCA GCA AAA CCT ATA AAT GGA AAA ACT GGA AAG GAA CAA CTT CCT GTA GGG TCA AAA L P P Q S A K P I N G K T G K E Q L P V 2221 TCT TTT GGG GTT ACT AAT ACG CGT GAT GAT GGG GAG AAT TCA ATA ACT GGA ACT GCT CCT CCT GTA GAT GGC V T N T R D D G E N S I T G T A P P P F 2296 AAA TTA ATT ATA ACCT TCA CCA CAA GTT TCT ATT CCC TCC CCT GTA CTT ATT CCG GCA CAA GAA GTA CAT ACT Q V S I P S P V L I P A Q E V H T KLIIKPSP ATT TGT AAT TAT GAA GGA ATT AGT GTT CAA ATT AAA CAT TCT TCT CCA TTC TCT GGC GTT GTT TTT GTT CGA AAT Y E G I S V Q I K H S S P F S G V V F V AAA TAT GAT ACT TGC CGT GTG AAG TTG AAG GAA AGG ACA GCG TTG TTT TGG TTT TGG GGC TTC CAG CAA ATT TTG K Y D T C R V K L K E R T A L F W F W G F Q 2521 GAA ATG AAG CCA ATT GCT TTA ATT AAT TCA CAA AAA CAT GGA AAA GGG AAT AAA ACA CAC GGA GAT ACT TTA CTT E M K P I A L I N S Q K H G K G N K T H G D T L 2596 TCT ATT GAA GGT TCC AAA AAA CAA ATT GAA GGG GGT TCT TCA ACT GAA GAT ATT CAA TTA ATA AAT TCT CAA AAA S I E G S K K Q I E G G S S T E D I Q L I N 2671 GAC CTT AAA CGT TCA AGA AGA CAA TTA CAA AGA GAT TGT GGA TTA CAA GAT ATG GAC AAT GGA ACT TAC AAA ACT D L K R S R R Q L Q R D C G L Q D M D N G T GTT ATT GTT GTC CAA ACA AAT AAT TTG GGA ATT CCG GGA CTT GTT ACT TCT ATG GAC CAA CTT TAT GAG ATT TCC V Q T N N L G I P G L V T S M D Q L Y E I S 2821 TGT AAC TAT TCA AGT ATG TTG GGA GGC AAA GTC CAA ACA GCA GCT GCA TTA CGT GTT CAC GGT CCC CAA CCT TCA C N Y S S M L G G K V Q T A A A L R V H G P Q P 2896 CTA ATC CAG CCT CGC GGC AAA ATA GAA TTG GGA AAT CCT GTT TTG ATG CAA ATG GGG CCT GTA CGT AGT GAA AGG PRGKIELGNPVLMQMGPVR S L I 2971 CAA AGT GGG GAA GGG CCT TTA ATT CAA GCT AAA TTG GGG GAT ATT CTT GAA TTA AAA TGG GAA ATT ATG GCA ATG O S G E G P L I Q A K L G D I L E L K W E I M A 3046 GAT GAA GAA TTG GAC TTT TTA GTT CGT GAT TGT TTT GCA GAG CCG GGA ACT TCT GGA AAT CAA GGG GAA AGA CTT D E E L D F L V R D C F A E P G T S G N Q G E R

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CCT TTA ATT GAG AAT GGT TGT CCA ACA CCA GCA GTA GCA CAA AAA TTA ATT CCA AAT CCA ATA AAA GCA ATT AAT P L I E N G C P T P A V A Q K L I P N P I K A I N 3196 TCT GCA GTT AAA TTA ACT TAT TTA CAA GCA TTC AGA TTT GAC AGT TCT CCA GCT ATT AGA ATA ACT TGT CAT TTA S A V K L'T Y L Q A F R F D S S P A I R I T C H L 3271 GAA TTA TGT AAA GAA AAT TGT AAA TCG GTT AAT TGT AAA TTT AAT GGT GGA ATT AAA GAA TCG TGG GGC AGA AAA ELCKENCKS VNCKFNDGIKES WG 3346 CGC CGT TTT GCT ATT GAC AAT AAC ATT AAT AGG AAA AAT GAA GTT AAA GAA TTC GAA ACT CGC CGT TTT GTC GTT RRFAIDNINRKNEVKEFETRRF 3421 CCC CGT TTT GCC CAA GCA ACT TCT TTA GTT ATT GTA GAC CCT TTA CAA CAA CAA AAT TCT GTT ATA AAA ACA P R F A Q A T T S L V I V D P L Q Q N S V I K T 3496 GAA CAA CAA CAA CAA CCA TTT ATT TCA CAT TCC TCA ATA TCT AAA CAA ATA TTT GAA AAT AAT AAA AAA GAA AAT EQQQPFISHSSISKQIFENNKKEN 3571 AAT AAA AAT ATA ACA AAA ACA GCT AAA AAA TCC TCT TCT CTT TTT GAA GCT TTT ACT GAG GCT GCT GGT GGA AGG N K N I T K T A K K S S S L F E A F T E A A G G R AAA ATT AAT TTA GAA TTA ACA ACA ACA AAT TCA GAA CAA CAA CAA CTT TGT TTA CAT AAA TGG ACA CTT GGG GGT K I N L E L T T T N S E Q Q Q L C L H K W T L G G 3721 GTT TTT GGA ACT CTT TTA ACA TTA ATT GTT GTT CAA AGC GGG GTT GCT GCT AAA CAT TTA ATT AAT CGA TTT ATT V F G T L L T L I V V Q S G V A A K H L I N R 3796 GTT GGA AAA AGA ATT TAAaaaaaaaaaaaaaaagtactagtcgacgcgtggcc VGKRI

FIG. 3C

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GAG CAG AAG ATT TTG GTG GGT TTC GCG CGG GAG GTG GTC TCC GCC GAC TCA GTC CAC CGC TGT CTG
EQKILVGFAREVVSADSVHRCL
67
TCC GCT TGT CTG AAT GCG TTC GAT ACG TTC GGC TTC GAA TGC GAG TCG GTC ATG TAT TAC CCT GTG GAC GCG GAA
S A C L N A F D T F G F E C E S V M Y Y P V D A E
TGC ATT TTG AAC ACG GAG GAC CGA TTG GAT CGG CCT GAC CTT TTC GTG GAC GAG GAC GAG GAC ACG GTC ATC TAC
           TEDRLDRPDLFVDEHEDTVIY
CILN
217
TTG GAC AAC AAT TGC GCC GGA TGT GAG TGC CAT TGG CAT TTT GAC AAT TTC AAA ACA AGC GGC ATT TTG AAC GAC
L D N N C A G C E C H W H F D N F K T S G I L N D
292
CAA CAA TTC GCA ATT GCA GCA CAA TGT TAC GCA CCG TAC GTA ACG CAA TAC GTG GCG GTG GAA GGA CGC CAA TTG
Q Q F A I A A Q C Y A P Y V T Q Y V A V E G R
TCG GAC GAA TTG GAC CAC AGT TTT GAA GGG TTG GAG CTG AGC GAA TGT GAA GAG TTG TGC ACG CAA CGG TTA AGT
S D E L D H S F E G L E L S E C E E L C T Q R L S
GTT ACG GCA AAC GAC TTC AAC TGC AAA TCG TTC ATG TAC AGT AAC TTG ACG CGC AGT TGC GTT TTG TCG GAC GAA
V T A N D F N C K S F M Y S N L T R S C V L S D E
517
CGC TCG CGC CCT TTG GGC CGT GCC AAT TTG GCC GAA GTG CCG GGA TGG ACT TAT TTC GAG AGC CGC GGC GTT CCG
R S R P L G R A N L A E V P G W T Y F E S R G
TCG TTT ACG CGA GTG CCG CAA ATG CTT TTG GTG GGC TTT GCC TCT TTT GTG ATG GAA AAT GTG CCG TCA GTG ACA
S F T R V P Q M L L V G F A S F V M E N V P S V T
667
ATG TGT TTG GAC CAA TGC ACA AGC CCT CCT GAG ACG GGA CAA AAC TTT GTG TGT AAA TCG GTG ATG TAC TAC
M C L D Q C T S P P E T G Q N F V C K S V M
742
TAC AAC GAG CA
Y N E
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FIG. 4

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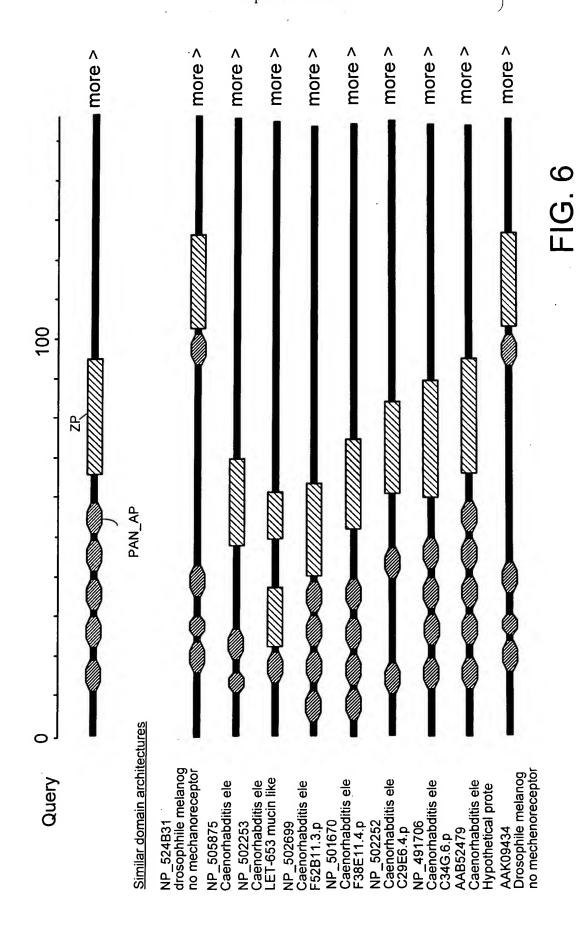
cgactggagcacgaggaccactgacatggactgaaggagtagaaaatttctgttgttcatttcttatcagactgtcccattcatcatcgtgaccactacca101 gtattacttcaggacagtaatattcgggtaaatttcggctgctcaatcggtaggaccgctttaat ATG CAT CTT TCC AAC CAT GCC TCA MHLSNHAS TCA CTT CTG CAT TAC TAT TCA CAT CTC ATC ATA ATT GCA TAC TTT TCT GTA TTT GCT TCA ATC GAA ATA CAA GAA S L L H Y Y S H L I I A Y F S V F A 265 ATT CCA TCA TAT CCA GCA TGT AGC AAT GGC GAA TCA CCT GTC TTT TTA CTC CAA CAC AAT GCT ACA GCA GGT AAT I P S Y P A C S N G E S P V F L L Q H N A T 340 GTT CTG AAG CGA GCT TCA ACT TCA CAT CTG GTC GAC TGC ACT GAC CTT TGT TCA GCT AAC GAT GAA TGT TTG GCG V L K R A S T S H L V D C T D L C S A N D E C L A ATA ACC TAT GAA GAT AAA GAA TGC AAA ATG TTG TCA AGC ATT GGA GAA TCG ACA GGA CAT TTA AAT GAT TAT GTA Y E D K E C K M L S S I G E S T G H L N D Y V T T 490 TTG CTG AGT AAA AAT TGT GCT AAA AGT GCG CGG ATC TGC TCA TCG CCA TTT CAA TTC GAT GTA CAC AGA CAA AAA L L S K N C A K S A R I C S S P F Q F D V H R Q K 565 ATT TTG GTT GGG TTT GCT CGC GAG GTT GTG TCA GCT GAT TCA TTA TCG TTA TGT CTA TCA GCT TGC TTG AAT GCA I L V G F A R E V V S A D S L S L C L TTT GAT TCT TTC GGT TTT GAA TGT GAG TCG GTA ATG TAC TAT CCA GTT GAT TCA GAA TGC ATC CTA AAC ACC GAA G F E C E S V M Y Y P V D S E C I L N T E 715 GAT CGT CTG GAT CGA CCT GAC TTG TTT GGG GAT GAA TTA GAT GAT AAC GTC ATT TAT TTG GAT AAC AAC TGT GCT D R L D R P D L F G D E L D D N V I Y L D N N C A 790 GGA TCA CAG TGT TAT GCT CCA TAC ATA ACA CAA TAC ATT GCC GTC GCA AAT CGT CAG CTA GCT AAC GAG TTG GAC G S Q C Y A P Y I T Q Y I A V A N R Q L A N E L D 865 AGA CAA CTG ATC GCT GAT CGT GAA TCA TGC GAG TCG TTA TGT ACT CAG CGA CTG TCT ACA ACG ACA AAC GAT TTC ADRESCES LCTQRLSTT AAC TGT AAA TCA TTT ATG CAT AAT CCG GAA ACT AAC GTT TGC ATA CTT TCT GAT GAA CGT TCT AAA CCA CTT GGT N C K S F M H N P E T N V C I L S D E R S K P CGA GGC AAT CTA GTG AAA GCT GAC GGT TTC ACA TAT TAT GAG AAG AAA TGT TTT GCA TCA CCA CGA ACA TGT CGC R G N L V K A D G F T Y Y E K K C F A S P R T C R 1090 AAT GTA CCG TCG TTT GAG CGC ATA CCT CAG ATG ATA CTT GTT GGT TTT GCT GCA TTT GTT ATG GAA AAT GTA CCT FERIPQMILVGFA-AFVM 1165 TCA GTA ACG ATG TGC CTC GAT CAG TGC ACA AAT CCT CCA CCG GAA ACT GGA GAA AAT TTC GAA TGC AAA TCT GTG S V T M C L D Q C T N P P P E T G E N F E C K S 1240 ATG TAT TAT TAT AAC GAA CAG GAA TGT ATT TTA AAC GCT GAA ACA CGA GAA AAT AAA TCG GAA TTG TTT ATA CCG M Y Y N E Q E C I L N A E T R E N K S E L F I P GAG GGA GAA GAA TTC CAA GTC GAT TAT TTT GAT ATC ACT TGT CAT CTG CGC CCT GAA ACA TGT CCA AAT GGC ACA F Q V D Y F D I T C H L R P E T C 1390 ACA TTA CAT ACT GTA CGT ACG GTT AAT GCA GCA CTC CCT GAA GGC GAA GGA TCG ATC CAT ATT TTG CAG TCA GCC T L H T V R T V N A A L P E G E G S I H I L Q 1465 GGG AAT TCG GTT GCT GAT TGC ATG ACA AAA TGT TAC GAG ATG GCT CCC GAG AAA TGT CGC GCA TTC AAT TTT GAT G N S V A D C M T K C Y E M A P E K C R A F N F D

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1540 AAG CAG ACA TCT GAC TGT GAC CTG TAC GTT GAT GGG AAG ACA ACC TTA CGA CCA GCA GTC CAC TCG GGC ATT K Q T S D C D L L Y V D G K T T L R P A V H S G I 1615 GAT CTC TAC GAC CTT CAT TGC CTA GAG CAG ACA AAA GTT TGC GCT CAG AAA AAC AAC GTA ACA CGA TTT TCG AGA D L Y D L H C L E Q T K V C A Q K N N V T R F S R 1690 TAT TTG TAC AGT ATA TAT GAT GCA GTG CCA TCG CAA TTC TAC GAA GCA ACT GCC CTC ACA AAT TGT CTT AAT CTT Y E A T A L T N C L N L Y L Y S I Y D A V P S Q F 1765 TGC GCA TAT ACC GAG CGT TGC GAA GGT GTA AAT TAC AAC AGA AGG AAT GGT CGT TGT GAA TTA TTT GAT AAG GTC ERCEGVNYNRRNGRCELFD 1840 GAA GGA AAT GGA AAG CCA AGT GAT TTC ACG GAT TTT TAC AAA AAT CTT TGT CTG GTG GAA GAA GTA GAA TCA GAA E G N G K P S D F T D F Y K N L C L V E E V E S E 1915 TAT AGC GCC GCA GCT AAT GTT CCC AAA CAT CTC CTT CCG AAT GTT TCA CAT TCT GCA GTT ACT CAG AAA CAA GAA Y S A A A N V P K H L L P N V S H S A V T Q K Q E 1990 GCT AAA TTA CAC ATT ATC TCA GCA AAA ACA AAG CCT TTC CTA CGC GAA CAG GAA GCA CAG CGA CGA GCT CCA GAA AKLHIISAKTKPFLREQEAQRRA 2065 ACA ATA ACA GCG AAG TCG TCT TCA GCT TCC GGA AAA GTA AGT GGT GAA GCA GGA TCA TCA ACT ACA TTC AGC ATT T I T A K S S S A S G K V S G E A G S S T T F S I 2140 TCT TCA TCC GGA AGG CTT CCA GGG CCA GTA GTC CAA ATT GCT CCA AAT GCA GTG CAA ACA GTT TGC AAT TAT GAA V Q I A P N A V Q T V C N Y E S S S G R L P G P V GGC ATC AAA GTG CAG ATG GAG AAC CCC AAA GCC TTT TCG GGA GTG ATA TTT GTT AAA AAT AGG TAT GAA ACC TGT Q M E N P K A F S G V I F V K N R Y 2290 CGA GTA GAG GTT ACG GAT AGT GAA AGT GCA CCA CTA GTA ATT GGT TTA CCA CCG AAT TTT GGT TCA AAA ATG GTA R V E V T D S E S A P L V I G L P P N F G S K M V 2365 GCT GAT GAA AAG GTT GCC GCA AGC GAA GCA AAT ATT CAA CCA GAA ATA TCC GGA GGC GAC AAA CTG GAT AAA CCC A D E K V A A S E A N I Q P E I S G G D K L D K P GCT GAT GAA CTG CGC ATA AGA CGA CAA GCT TTA GAG CTA CAC AGA GAT TGC GGA ATC CAG GAT ATG AAC AAT GGT I R R Q A L E L H R D C G I Q D M 2515 ACT TAT AAA TCA ACG GTG GTT GTA CAA ACA AAT AAC TTG GGT ATA CCT GGA CTG GTA ACT TCC ATG GAT CAG ATT TYKSTVVVQTNNLGIPGLVTSMDQI TTT GAA GTG AGC TGT GAT TAT AGT TCA ATG CTT GGT GGA AAA GTT ACT GCT GGT GCC AAT CTC ACA ATT GAT GGT F E V S C. D Y S S M L G G K V T A G A N L T I D CCC GAA GCA TCT CTT ATT CAA CCC CGA GGA AAA ATC GAA CTT GGT AAC CCG GTG CTT ATG CAG ATG TTG AGT GGA A S L I Q P R G K I E L G N V L 2740 CAA GGA GAA CCT GTC CTA CAA GCA AAA CTA GGT GAC ATT CTG CAG CTA CGA TGG GAA ATC ATG GCG ATG Q G E P V L Q A K L G D I L Q L R W E I M A M

FIG. 5B

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126	101 101 101 112 118	232 224 2234 223 216 224	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 8 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
SEQ_ID_NO_10 MVTKIPTPPLLFIFPFLFTTKCQAYSIPLISECNSEEAPVFLLQRNVSSIAGTEPLRTVPVTGGFLECAELCSAANNCVAVKFSIEKQCQLLGKTTMTATTLSLQDINLTLARLATKSCVKSK	SEQ_ID_NO_11 SEQ_ID_NO_11 SEQ_ID_NO_11 SEQ_ID_NO_12 SEQ_ID_NO_14 SEQ_ID_NO_15 SEQ_ID_NO_15 SEQ_ID_NO_16 SEQ_ID_NO_17 SEQ_ID_NO_17 SEQ_ID_NO_17 SEQ_ID_NO_19 SEQ_ID_NO_17 SEQ_ID_NO_19 SEQ_ID_NO_17 SEQ_ID_NO_19 SEQ_ID_NO_17 SEQ_ID_NO_19 SEQ_I	SEQ ID NO 10 KICSSPFHFDVHEQKILVGFAREVVSAESIHQCLTACLDAVDTRGFECESVMYYPLDAECTILNTEDRIDDRPDLFVDEKEDTVVYLDNNCAGSQCHAPYVTQYVAVE SEQ_ID_NO_11EQKILVGFAREVVSADSYHRCLSACINAPDTRFFECESVMYYPUDAECTILNTEDRIDDRPLEFEDTVIYIDNNCAGCECHWHPDNFKTSGILNDQFALAACYAPPYTQYVAVE SEQ_ID_NO_12	SEQ ID NO 10 GRQLABELDHNFEGMELTECEQLCRQRLSVSANDFNCKAFMYNNQTRSCILSDERSRPLGRANLTDAKGWTYHEKKCFASPRTCRNVPSFTRVPQMLLVGFASFVMENVPSVTMCLDQCTNPPPETGQSF SEQ_ID_NO_11 GRQLSDELDHSFEGLELSECEELCTQRLSYTANDFNCKSFMYNNGTRSCILSDERSRPLGRANLTDAFGYTYFEKKCFASPNTCRNVPSFTRVPQMLLVGFASFVMENVPSVTMCLDQCTSPPETGQRP SEQ_ID_NO_17 GRQLKNELDR -IINVDLDSCQALCTQRLSISSNDFNCKSFMYNNKTRTCILADERSKPLGRADLIATEGFTYFEKKCFASPNTCRNVPSFKRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGDGF SEQ_ID_NO_17 GRQLKNELDR -IINVDLDSCQALCTQRLSISSNDFNCKSFMYNNKTRTCILADERSKPLGRADLIATEGFTYFEKKCFASPNTCRNVPSFKRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGGGF SEQ_ID_NO_18 GRQLKNELDR -IINVDLDSCQALCTQRLSISSNDFNCKSFMYNNKTRTCILADERSKPLGRADLVATEGFTYFEKKCFASPNTCRNVPSFKRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGGGF SEQ_ID_NO_18 GRQLKNELDR -IINVDLDSCQALCTQRLSISSNDFNCKSFMYNNKTRTCILADERSKPLGRADLVATEGFTYFEKKCFASPNTCRNVPSFKRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGGFF SEQ_ID_NO_18 GRQLKNELDR -IINVDLDSCCALCTQRLSISSNDFTCKSFMYNNFTRTCILADERSKPLGRALLSDAGFTYFEKKCFASPRTCRNVPSFKRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGGFF SEQ_ID_NO_18 INQIENELDR -IINVDLDSCCALCTGRITYTONDFTCKSFMYNPTRTCILADERSKPLGRAKLSDAGFTYFEKKCFASPRTCRNVPSFRRVPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGERF SEQ_ID_NO_18 INQIENELDR -IINVDLDSCCALCTGRITYTONDFTCKSFMYNPFTKVCYLSDAGFTYFEKKCFASPRTCRNVPSFRRIPQMILVGFAAFVMENVPSVTMCLDQCTNPPPETGERF SEQ_ID_NO_180270270310310310	********* SEQ ID NO 10 VCKSVMYYNEQECILNAESRHSKPDLFIPEEDDFVVDYFDINCRLEQEQCIDGRTPQLVRTINSALPEGEGSIHVLET-IKGGVQQCAKKCSERAPDKCRSFNFDKQACNCNLLYLDGQGSLRPEQKTQ SEQ ID NO 11 VCKSVMYYNEQECILNSETRESKPELFIPEGEEFLVDYFDITCHLKQEKCPTGQHLKAIRTINAALPEGESELHVLKASAAKGIKECVAKCFGLAPEKCRSFNYDKKTKSCDLLYLDGHNTLQPQVRQG SEQ ID NO 17 VCKSVMYYNEQECILNSETRESKPELFIPEGEEFLVDYFDITCHLKQEKCPTGQHLKAIRTINAALPEGESELHVLKASAAKGIKECVAKCFGLAPEKCRSFNYDKKTKSCDLLYLDGHNTLQPQVRQG SEQ ID NO 17 VCKSVMYYYNEQECILNSETRESKPELFIPEGEEFLVDYFDITCHLKQEKCPAGGHLKAIRTINAALPEGESELHVLKSSAAKGIKECVAKCFGLAPEKCRSFNYDKKTKSCDLLYLDGHNTLQPQVRQG SEQ ID NO 45 VCKSVMYYNEQECILNSETRESKPELFIPEGEFLVDYFDITCHLKQEKCPAGGHLKAIRTINAALPEGESELHVLKSSAAKGIKECVAKCFGLAPEKCRSFNYDKKTKSCDLLYLDGHNTLQPQVRQG SEQ ID NO 45 VCKSVMYYNEQECILNAETRESKPELFIPEGEFLVDYFDITCHLKAPERTKSTKINTINAALPEGESELHVLKSSAAKGIKECVAKCFGLAPEKCRSFNYDKKTKFSCLLYLLYDFANTLGPTKOF SEQ ID NO 45 VCKSVMYYNTEGECILNAETRENKSELFIPEGEFTONFTHLAVVAAALPEGEGSLHVLKSSAAKGIKECMAKCNQLHPEKCRSFNYDKKTKFPTKNTTKPFTKNG SEQ ID NO 45 VCKSVMYYNTEGECILNAETRENKSELFIPEGEFTONFTHLAVVAAALPEGEGSLHVLKSSAAKGIKECMAKCNQLHPEKCRSFNYDKGTSTLKAPFTNAG SEQ ID NO 45 VCKSVMYYNTEGECILNAETRENKSELFIPEGEFTONFTHLAVVAAALPEGEGSLHVLKSSAAKGIKECMAKCNQLHPEKCRSFNYDKGTSDCDLLYVDABAUFGG TU A100

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•	-	
614 559 592 592 591 592 587	691 250 634 638 637 667	794 250 715 719 718 771
SEQ_ID_NO_10 FDLYDVHCLSGTSQLLGENSKHSPSACVDPEGAIFSRFLYTRWVANSPNREISSLPLSKCLNLCSVGGEQCEGVNYNRRNGSCQLFTSLLLNSSPNSQQDKDEHVDFYRNICTVKEIDTGASASCEOTD-NO-11	SEQ_ID_NO_10 ANVDKTQQAT	SEQ ID NO 10 ENSITGTAPPP SEQ ID NO 1 ENGITGTAPPP SEQ ID NO 1 ID NO 1 SEQ ID NO 16 ID NO 16 SEQ ID NO 16 ID NO 16 SEQ ID NO 17 ID NO 17 SEQ ID NO 18 ID NO 19 SEQ ID NO 45 ID NO 45 SEQ ID NO 45 ID NO 45

FIG 7B

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918 250 823 827 826 873 850	20045 20045 995 896 891	1175 250 1030 1034 1033 1085 881	
	H		
SEQ ID NO 10 KGNKTHGDTLLSIEGSKKQIEGGSST-EDIQLINSQKDLKRSRRQLQ-RDCGLQDMDNGTYKTVIVVQTNNLGIPGLVTSMDQLYEISCNYSSMLGGKVQTAAALRVHGPQPSLIQPRGKIELGNP SEQ_ID_NO_11	SEQ_ID_NO_10 VLMQMGPVRSERQSGEGPLIQAKLGDILELKWEIMAMDEELDFLVRDCPAEPGTSGNQGERLPLIENGCPTPAVAQKLIPNPIKAINSAVKLTYLQAFRFDSSPAIRTTCHLELCKENCKSVNCKFN SEQ_ID_NO_11GDGTEQPLOVAKLGDILELKWEIMAMDDELDFPVKNCHAEPGVAGGKAGAGEKLRLIDGGCPTPAVAQKLIPGAIEIKSSAVKTTKMQAFRFDSSASIRVTCEVEICKGDCEPVECALT SEQ_ID_NO_15 VLMQLLNGDGTEQPLVQAKLGDILELKWEIMAMDDELDFPVKNCHAEPGVAGGKAGAGEKLRLIDGGCPTPAVAQKLIPGAIEIKSSAVKTTKMQAFRFDSSASIRVTCEVEICKGDCEBVECALT SEQ_ID_NO_45 VLMQLLNGDGTEQPLVQAKLGDILELRWEIMAMDDELDFPVKNCHAEPGAGEKLQLIDGGCPTPAVAQKLIPGAIEIKSSAVKTTKMQAFRFDSSASIRVTCEVEICKGDCEAVECALT SEQ_ID_NO_45 VLMQMNAGTGDHQPILGAKLGDILELRWEIMAMDEELDFFVKDCHAEFGTGAGGDEKLQLIEGGCPTPAVAQKLIPQPIKLQSSAVKTTKMQAFRFDSSSSVRITCNIEICKGDCKAVCTGATCANT SEQ_ID_NO_3 VLMQMNAGTGDHQPILQAKLGDILGARWEIMAMGTGDERQFLQAKLGDILGARWEIMAM	SEQ_ID_NO_10 DGIKESWGRKRRFAIDNINRKNEVKEFETRRFVVPRFAQATTSLVIVDPLQQQNSVIKTEQQQQPFISHSSISKQIFENNKKENNKNITKTAKKSSSLPEAFTEAAGGRKINLELTTTNSEQQQLCLHK SEQ_ID_NO_11 SEQ_ID_NO_16 GGVKKSFGRKKREVSNN	FIG. 7C
SQKDLA EIEEFF EIEEFF EIEEFF GHKVVC DELRIF 50	EELDFI DELDFI DELDFI EELDFI 80	AQATTS SHATTS SHATTS SHATTS SQATTS	1210 250 1065 1069 1122 1122 881
0 KGNKTHGDTLLSIEGSKKQIEGGSST-EDIQLIN 1	1 U. VLMQMGPVRSERQSGEGPLIQAKLGDILELKWEIMAMD. 1 VLMQLLNGDGTEQPLVQAKLGDILELRWEIMAMD. 1 VLMQLLNGDGTEQPLVQAKLGDILELRWEIMAMD. 2 VLMQLLNGDGTEQPLVQAKLGDILELRWEIMAMD. 3 VLMQMNAGTGDHQPILQAKLGDILELRWEIMAMD. 2 VLMQMNAGGGEPVLQAKLGDILELRWEIMAMD. 3 VLMQMNAGGGEPVLQAKLGDILELRWEIMAMD. 5 VLMQMLSGGGEPVLQAKLGDILGLRWEIMAMD. 6 VLMQMLSGGGEPVLQAKLGDILGLRWEIMAMD. 6 VLMQMLSGGGEPVLQAKLGDILGLRWEIMAMD. 7 VLMQMLSGGGEPVLQAKLGDILGLRWEIMAMD. 7 VLMQMLS	O DGIKESWGRKRRFAIDNNINRKNEUKEFETRRFUVPRR. G GGWKKSFGRKKREVSNNIEEFETNRYLIPRR. G GGWKKSFGRKKREVSNNIEEFETNRYLIPRR. G GGWKKSFGRKKREVSNNIEEFETNRYLIPRR. G GGWKKSFGRKKREVNNNITEPETNRYLIPRR. Z	SEQ_ID_NO_10 WTLGGVPGTLLTLIVVQSGVAAKHLINRFIVGKRISEQ_ID_NO_11
SEQ_ ID_NO_1	SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_4 SEQ_ID_NO_6 SEQ_ID_NO_7 SEQ_ID_NO_1 SEQ_ID_NO_1	SEQ_ID_NO_10 SEQ_ID_NO_11 SEQ_ID_NO_17 SEQ_ID_NO_17 SEQ_ID_NO_45 SEQ_ID_NO_3 SEQ_ID_NO_3 SEQ_ID_NO_3 SEQ_ID_NO_3	SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_1 SEQ_ID_NO_4 SEQ_ID_NO_4 SEQ_ID_NO_7

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129	258	388	518	648	
128	257	387	517	647	
130	260	383	383	457	
SEQ_ID_NO_46 -MSPRVIELLGSFLTAQNYPECSSETTAFVRIPERELDGTPVVISTAGHDLTCAQYCRNNIEPTTGAQRVCASFNFDGRETCYFPDDAATPAGTSQLTANPSANNFYYEKTCIPNVSAHEACTYRSFS SEQ_ID_NO_18 -MWG-VIFLLESIVPAAQSVPECSSHETTAFVRIPRARLDGTPVVISTAGHDLTCAQYCRNNIEPTTGAQRVCASFNFDGRETCYFPDDAATPAGTSGLTANPSANNFYYEKVCIPNVSAHEACTYRSFS SEQ_ID_NO_4 MNWLSIASICTFLIIPISAYFECSGSETTAFIRISRARLDGTPVVISTAGHDLTCAQYCRNNIEPTTGAQRVCASFNFDGRETCYFPDDAASPAGTGELNEAPSANNFYYEKVCLPAISAHEACTYRSFS SEQ_ID_NO_4 MNWLSIASICTFLIIPISAYFECSGSETTAFIRISRARLDGTPVVISTAGHDLTCAQYCRNNIEPTTGAQRVCASFNFDGRETCYFPDDAASPAGTGELNEAPSANNFYYEKVCLPAISAHEACTYRSFS SEQ_ID_NO_46 MNWLSIASICTFLIIPISAYFECSGSETTAFIRISRARLDGTPVVISTAGHDLTCAQYCRNNIEPTTGAQRVCASFNFDGRETCYFPDDAASPAGTGELNEAPSANNFYYEKVCLPAISAHEACTYRFFS SEQ_ID_NO_46 MNWLSIASICTFLIIPISAYFECSGSETTAFIRISRARLDGTPVVISTAGHDCACTORNIEPTTGAGRACTORNIEPTTGAGGRACTORNIEPTTGAGGRACTORNIEPTTGAGGRACTORNIEPTTGAGGRACTORNIEPTTGAGG	***: *********************************	***; *************; *********; ********	SEQ ID NO 46 GMALCTNEGIRFIVNTKEPYTGAIYAAERFSTCSQVVENAKQISITFPPPTVTSDCGTVIRDGKMEALVVVSLDGVLPHQVTTEWDRPYRVSCDVSMDKMVKEGSVVVTTIYEASSQNTTVLDVATPPPV SEQ_ID_NO_18 GMALCTNEGIRFIVNTKEPYTGAIYAAERFSTCSQVVENAKQISITFPPPTVSSDCGTVIRDGKMEALVVVSLDGVLPHQVTTEWDRFYRVSCDVSMDKMVKEGSVVVTTIYEASSQNTTVLDVATPPPV SEQ_ID_NO_4	SEQ ID NO 46 TAELQILNQLEEPLHKASIGDPLLLVITSEQAGPHNMMVTECTATRVGGFGDTVPFTLIENGCPRYPALVGPVEQDFDKNRLKSDLRAPRLDGSYDVQIVCSIMFCAGPNGCPVSNCLDSGTNELFMSHG SEQ_ID_NO_18 SAELQILNQLEEPLHKASIGDPLLLVITSEQAGPHNMMVTECTATRVGFGDTVPFTLIENGCPRYPALVGPVEQDFDKNRLKSDLRAPRLDGSYDVQIVCSIMFCAGPNGCPVSNCLDSGTNELFMSHG SEQ_ID_NO_4	SEQ_ID_NO_46 RKRRS-VDLEAGET-EERLSAIIRVFAKGEDEEEIEMG-NNTLMTSLAESTDL.CIAEDFFVSSVVSLSVLCFALSAIIAIWGCHALHAKPTKQVAA 742 SEQ_ID_NO_18 RKRRS-ADLEAGET-EEKLSAIIRVFAKGEDEEENEMANNTMMTSMSDSTELLCIAEDFFVSSVVSLSVLCFALSAIIAIWGCHSLHSKPVKQVAA 741 SEQ_ID_NO_4 RKKRS-VDREAGET-EEKLSAIIRVLAAGEEELEVEFFYNDTNFKYDSEENISAHNLYCMSEMFVSGIVSMAMICLLLSUVWHGCHSLHQSSKLPM 557 SEQ_ID_NO_4 RKKRSIVDPKNTTTSATELSAIIRVLAAGEEELEVEFFYNDTNFKYDSEENISAHNLYCMSEMFVSGIVSMAMICLLLSUVWHGCHSLHQSSKLPM 557 FIN A REPAIR OF THE PROPERTY SET OF TH